CRF Error Corrected by th STIC System Branch

Serial Number: _10/020,695_

ENTERED

CRF Processing Date: _1/15/2002_
Edited by: _A_
Verified by: _AV_ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.   #2

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: Th above corrections must be communicated to th applicant in the first Office Action. DO NOT send a copy of this form.   3/1/95

OIPE

RAW SEQUENCE LISTING   DATE: 01/15/2002
PATENT APPLICATION: US/10/020,695   TIME: 16:55:53

Input Set : **A:\pto.amc**
Output Set: **N:\CRF3\01152002\J020695.raw**

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  1 <110> APPLICANT: KIM, Dong-Soo
  2         NAM, Yoon-Kwon
  3         NOH, Jae-Koo
  5 <120> TITLE OF INVENTION: EXPRESSION VECTOR CONTAINING LECTIN GENE REGULATION SITE OF
MUD
  6         LOACH
  8 <130> FILE REFERENCE: PPBA0566
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/020,695
C--> 10 <141> CURRENT FILING DATE: 2001-12-12
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 12 <170> SOFTWARE: KopatentIn 1.71
 14 <210> SEQ ID NO: 1
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 16 <212> TYPE: DNA
 17 <213> ORGANISM: Misgurnus mizolepis
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 24 ccttcctccg gcgtacagga gggttcaccc tgtgttccac gtctccaata ttaaaccggt       180
 26 gattttttcc cgtcttaatc cgcctgcccc ggttcccccc ccgcctcgtc tcgttaatgg       240
 28 ggaaccgact tattcggtta atcgtattct ggactccaga cggaggggac gcggatttca       300
 30 gtacttggtg gattgggaag gttacggtcc ggaggagaga aggtgggttc ctgctcggga       360
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 40 taaatactca catgactctc tgttccctgc cagatgatca ctttctgttt ggtcctcgtg       660
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 44 tagtcgtctt cgtgtggatg ttccgtgtac agtctggatt caccactgct caccactcca       780
 46 ccaacgccgc actcaataac cacctaccac cgtagtcctc gtcaccattg ccaacaacac       840
 48 cggacatttc ctgcttgtgt catttctctc tttgtgttta taaataaaca ttgtgttttc       900
 50 acctgcaatt gcttccgctc agttcgtgtc attacaagta cctcaaaata catattagta       960
 52 tctcaaaggt acatattgct actaaatgtt tacacatctg tacctaatgg tccatacaat      1020
 54 taccttttta aagggtgctg ccccagtgac agctagggta catattttga cttttttcta      1080
 56 acaatgtagg tcctaaaggt acggtaggct aatctaccca aaattgtatt ctgttttgta      1140
 58 ttcctgtagg taccaaacag aaacttaggg tacagcccca gtgacagaaa aggtacagtt      1200
 60 ttgtacctta atttctgaca atgaacgata aacaagaata actaaacac taccaaatga      1260
 62 tactaaaaac gaaagcataa aaaagatgaa aactaaaatg caaagaaaag aaaactgaag      1320
 64 tgactgagtt aaatttatgg cagaatgttt cctgtttctg ataagatgaa aaccttactt      1380
 66 ctaataaccc aaataaccaa ataattatct gcaaacatta aagaaactca gttatgcaat      1440
 68 ctatggtaaa tagttactga aagaatacac caatgccaag gttttttgggc aagaggtttg     1500
 70 tttacatgat atttacttt tgtgtggtca gatgagctgt ccggtggtgg gcccgtcggc      1560
 72 catggttcag gcttttacgt gctgcaaatg ggaatgagtc aggttcagtt caacagcctt      1620
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 78 tgagtcaact aatatttta agttgaatga actcaaaatt ttaagtcgct tttttaagttg    1800
 80 aaacatttct ttaccgttta tatcaagcag actgcaataa aactcttaca aaaatgcttc    1860
 82 tttgcatgat cacacacatt aaagaaacac actaaaaata caaaaataaa caaatctata    1920
 84 tatgcaatat atttatataa aatacttgca ataaacagta aaataacaaa atctaatgta    1980
 86 aagacatgag tcaataaaaa tatgtaaaac atccataaat gtaaaatata ctgaaagaaa    2040
 88 tgtgaacaca gaaaagtgtt catgtgtcag atcaggatgt ttattttgat aaccatcaca    2100
 90 tttcatcata tattgtatac atatatacaa gttcatgata tccagattta cttttcttgt    2160
 92 ttatgttatg gagtccctcc cactgaacaa aagtataaaa gataggactc ctcattgacc    2220
 94 atcacacaat ctacactgaa gttctgaaag tgaagatttg acaaaaaggt gagttttat     2280
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129 aaacttgctc ccaaatttat tggcccgttt tctgttacca agatcattaa tccggtaaca     180
131 gtgcgtctga gccttcctcc ggcgtacagg agggttcacc ctgtgttcca cgtctccaat     240
133 attaaaccgg tgattttttc ccgtcttaat ccgcctgccc cggttccccc cccgcctcgt     300
135 ctcgttaatg gggaaccgac ttattcggtt aatcgtattc tggactccag acggagggga     360
137 cgcggatttc agtacttggt ggattgggaa ggttacggtc cggaggagag aaggtgggtt     420
139 cctgctcggg acatactgga tcaccgcctt atcgatgttt acaatcaaca ggtaaagcag     480
141 gctgggaacg tcaaggggcg ttcctagggg aggggtact gtcacggtag gaaatcctct     540
143 gtttcctccg tgtcatgttt gtgtgtgtgt gtgtttgtta ctctctgctc tgccatgtgc     600
145 tcgttaggct gatgtcgctc acctgtgtgt tgattgcctc gctccagctg ctcatcatta     660
147 catctcctcc ataaatactc acatgactct ctgttccctg ccagatgatc actttctgtt     720
149 tggtcctcgt gttgtgtggt tctacgtctc agtcttggat tacgagttgc attgtggatt     780
151 gtttattgtc gtagtcgtct tcgtgtggat gttccgtgta cagtctggat tcaccactgc     840
153 tcaccactcc accaacgccg cactcaataa ccacctacca ccgtagtcct cgtcaccatt     900
155 gccaacaaca ccggacattt cctgcttgtg tcatttctct ctttgtgttt ataaataaac     960
157 attgtgtttt cacctgcaat tgcttccgct cagttcgtgt cattacaagt acctcaaaat    1020
159 acatattagt atctcaaagg tacatattgc tactaaatgt ttacacatct gtacctaatg    1080
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Output Set: N:\CRF3\01152002\J020695.raw

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163 actttttttct aacaatgtag gtcctaaagg tacggtaggc taatctaccc aaaattgtat      1200
165 tctgttttgt attcctgtag gtaccaaaca gaaacttagg gtacagcccc agtgacagaa       1260
167 aaggtacagt tttgtacctt aatttctgac aatgaacgat aaacaagaat aactaaaaca       1320
169 ctaccaaatg atactaaaaa cgaaagcata aaaaagatga aaactaaaat gcaaagaaaa       1380
171 gaaaactgaa gtgactgagt taaatttatg gcagaatgtt tcctgtttct gataagatga       1440
173 aaaccttact tctaataacc caaataacca aataattatc tgcaaacatt aaagaaactc       1500
175 agttatgcaa tctatggtaa atagttactg aaagaataca ccaatgccaa ggttttgggg       1560
177 caagaggttt gtttacatga tatttacttt ttgtgtggtc agatgagctg tccggtggtg       1620
179 ggcccgtcgg ccatggttca ggcttttacg tgctgcaaat gggaatgagt caggttcagt       1680
181 tcaacagcct tgaacacgaa gtgatgtgaa atgctgatca gctgttcagc ttaaaaaaag       1740
183 ttcatttgct gccttaaaat ccaacttttaa aatattagtt gacacaaaca gttttaaaca      1800
185 gtttctcgtt ttgagtcaac taatattttt aagttgaatg aactcaaaat tttaagtcgc       1860
187 tttttaagtt gaaacatttc tttaccgttt atatcaagca gactgcaata aaactcttac       1920
189 aaaaatgctt ctttgcatga tcacacacat taaagaaaca cactaaaaat acaaaaataa       1980
191 acaaatctat atatgcaata tatttatata aaatacttgc aataaacagt aaaataacaa       2040
193 aatctaatgt aaagacatga gtcaataaaa atatgtaaaa catccataaa tgtaaaatat       2100
195 actgaaagaa atgtgaacac agaaaagtgt tcatgtgtca gatcaggatg tttattttga       2160
197 taaccatcac atttcatcat atattgtata catatataca agttcatgat atccagattt       2220
199 acttttcttg tttatgttat ggagtccctc ccactgaaca aaagtataaa agataggact       2280
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205 tgttcattca ttttcagatt catc        atg gca gtc atg aga gct ctt gtg       2448
206                                   Met Ala Val Met Arg Ala Leu Val
207                                    1               5
209 ctt ctt ttc ttg gtc ttt tct gtt gag agt gca cca ggt           aac       2490
210 Leu Leu Phe Leu Val Phe Ser Val Glu Ser Ala Pro Gly
211      10              15                  20
213 caagacgttt acaagattga ccaaaccctg ttaccaatat tccagattaa attcccataa       2550
215 aattgtgttt tccataaaac ttgttaaaca ttataaacat catgaaagga tgtcaacaga       2610
217 agcaacattt aaagcactta tagacagaaa cataaaacta ataatgtgac tttatattac       2670
219 taatatttta atcactgtat agct        cat cgc tgc cca cat gga tgg aca       2718
220                                   His Arg Cys Pro His Gly Trp Thr
W--> 221                              1               5
223 ccc ttt ggt gtg caa tgc tac aaa ttc ttc tct cag tca gtt gac tgg       2766
224 Pro Phe Gly Val Gln Cys Tyr Lys Phe Phe Ser Gln Ser Val Asp Trp
W--> 225      10              15                  20
227 atc aca gct gag    gt actgttattc agttattcaa attgttgaat aagaatactc      2820
228 Ile Thr Ala Glu
W--> 229  25
231 aatgtcatga tccaagctga aacagattag attttatatt tgcaataaaa taatctctct       2880
233 ctctttag    aaa aac tgt caa tct att gat gct aat ctt gca tct gtg cgc     2930
W--> 234              Lys Asn Cys Gln Ser Ile Asp Ala Asn Leu Ala Ser Val Arg
W--> 235              1               5                   10
237 agt aca atg gaa cac aac ttt ctc ctg agt ctg att gtg tct gct aac       2978
238 Ser Thr Met Glu His Asn Phe Leu Leu Ser Leu Ile Val Ser Ala Asn
W--> 239  15              20                  25                   30
241 aca cgt gtt tgg att ggt ggc cat gat ggt gaa act gtaagt cattttgctc    3030
242 Thr Arg Val Trp Ile Gly Gly His Asp Gly Glu Thr
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Input Set : A:\pto.amc
Output Set: N:\CRF3\01152002\J020695.raw

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W--> 243              35                   40
     245 tgaaatgctg atattgtcat ggctagtctg aaattaatgc tttaattata aaactgattt   3090
     247 ttctatagat acaataacta aatgcttttt gttacaatat aaatgattga attatatcat   3150
     249 aaatgaaaag attattagta aactctttga ctctcctcac tcattag    gaa gga caa   3206
     250                                                        Glu Gly Gln
W--> 251                                                         1
     253 tgg ctg tgg tct gat gga tct caa ttt cac ttt acc aac tgg tgc cct      3254
     254 Trp Leu Trp Ser Asp Gly Ser Gln Phe His Phe Thr Asn Trp Cys Pro
W--> 255      5                   10                  15
     257 gga gaa cct agc aat aat ttt ggt aaa gag aac tgc ctg gag ata aac      3302
     258 Gly Glu Pro Ser Asn Asn Phe Gly Lys Glu Asn Cys Leu Glu Ile Asn
W--> 259  20                  25                  30                  35
     261 ttt aca cgt aagaaagtc tcatatcatt attgttttta tttacaatct taaaattcta   3360
     262 Phe Thr Arg
     264 tagcattttg tattaaattt acttgtttaa tgtcagaaaa tgctacgtgc agtgtattca   3420
     266 ctacattcag atccctttaa cctttcagtg ttgttatttt gcagcctgat ggtacaattg   3480
     268 tttgaattca tacttggttc cccataatga aaaagtgaaa acagaatttt ataaatgtct   3540
     270 gtaaaaaatt ttaaaagaaa aaatgtcaca tttactgtat ttaaaccaag ggtgccaaac   3600
     272 tctgtcttgg agggccggtg gtgacctgtg tagtttagct ctaacactaa tcaaacacac   3660
     274 ctaaagcagt ttattaaagt ctaactaagc atactagaaa cttctagaca ggtgagctga   3720
     276 gacaagttga aactaaactc tgcaggacac cgggcctcta ggaacgagtt tgggcacccc   3780
     278 tgatttagac cctttgcaac aacacttgaa attttgctca gatgcctctt gatcgttgct   3840
     280 gatttataca tttattttta ttcaaactac accggtaatg atcagtactg attttatttt   3900
     282 catcttatcc cacagag    aac cgt tgc tgg aat gat gcg gat tgt tca acc    3950
     283                     Asn Arg Cys Trp Asn Asp Ala Asp Cys Ser Thr
W--> 284                        1           5                   10
     286 aca atc agc tac att tgt gcc caa cct att aga tca    tgaa aaatcaatct   4000
     287 Thr Ile Ser Tyr Ile Cys Ala Gln Pro Ile Arg Ser
W--> 288              15                  20
     290 gtttcaaagt actatgattt tactacatgc ctatacattt ttttctgatc ttattcttaa   4060
     292 aactcagtat cttactgaag ctttctgaaa acttctccaa tcaataaaag catttataaa   4120
     294 gcaaattgtt tgcattgttg agtcaaaaaa attaatcatc aaattaaata caatataaaa   4180
     296 caaaacaaca atacatctaa aataacaaaa agggctttca caattgaaat agttaacctc   4240
     298 aggttattct aaaccccagg tttaaagaat cctgggttat ctgtttcacg tttcacactg   4300
     300 ttcatactta accaggaggt aaagaaataa ccctgggtat tcataatctg atgtttcaca   4360
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     304 taaggaagtt tcttcacctc ctcattagca tccagacagc agaagtaggg aactgagcag   4480
     306 cgttcatgac tgaggttctc ttcagaacaa ctgaagtaca ttgagactaa tccatgtaag   4540
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     310 accggggccc cccatgcccc agcattgccc aaggttttc atttgaattg cacaacaata   4660
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     314 gcttaaagta acactaaatt gttacagtat gacaaagatt cttatagatt catatataga   4780
     316 tgtcttagga tgtatttaaa acaatgtaat taatactgca acttcagtgt ctgacatctt   4840
     318 actaaaaaaa ctaaatgagg aaaaagagga agcattagat tatgattcag actggtctaa   4900
     320 caaacaccag caaacaatat tgtaagttgg ttaatgcttg acttaatgga tgggaatcac   4960
     322 ataactctca tgttcatatt gcaaaacaa acttactgtg agatacaaca agcatataga   5020
     324 ctagacatac actaaagatg agattttaat gacaatgatg agatacagaa tatgatttat   5080
     326 gtattttcga catgtgtggt gtctttatca tgttaatacc tgtacgagca tggaacaaaa   5140
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334 tactcacaca tctctccctc gcacgtgctt tatccgtacc ttagatttgg ttctgaataa    5380
336 acctaacata ctttcgcaca ccttgtggcc agtagggggc ccccaagcct gcgggcccta    5440
338 cgcaattgca tggtttgcgt ggtgggtaaa cacgccactg gttacattgc aagatacttt    5500
340 gtaaaaaat gttaatctgt taatagtgcc ctattttaac aatctaagtg catggtctaa     5560
342 agtgcaaaag ggtttgtcct aatccacttc tgctaattta acgacgggac aaattttggg    5620
344 gcgtctagcg cactgtctta aagggttgtt cctattctag taatgagtaa tgggtgtgtt    5680
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350 acgaacagtg attgttgatt tgtatgtgca tcaaggcaag gcaagtttat ttgtatagca    5860
352 catttcatac acagaggtca ttcaaggtgc tttacataga aatgagaaaa caatatatga    5920
354 gaaaaaagt atgtagaaaa aaatcaaaga tacatttgaa tttaaaatat caattaaaag     5980
356 aaaataaatg tgattttaat agaaactgtt taaatgtgtg aaaaaaataa agtataaaac    6040
358 agtaaaaaaa aattattatt atttagctca gtgggaccat atacaggttg aacaggagtg    6100
360 cttcggacaa cctgacaatt gtcagaatag atcagagaat tgcctggaaa taaacttttg    6160
362 aagtaagaat gtctattatt attgttttta ttataatctt aacattttat aggatttagt    6220
364 acacaataag ccagtttagc tgtcagaaaa tgttacgtgc agtgcattca ctacattcag    6280
366 atcccttca tttttttttt ttcaatgttg tgtagtgatt ttgacacgag caccaattaa    6340
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380 ggattgttta ttgtcgtcgt cgtcttcgtg tggatgttcc gtgtacagtc tggattcacc    6760
382 actgctcacc actccaccaa cgccgcactc aataaccacc taccaccgta gtcctcgtca    6820
384 ccattgccaa caacaccgga catttcctgc ttgtgtcatt tctctctctg tgtttataaa    6880
386 taaacattgt gttttcacct gcaattgctt ccgctcagtt cgtgtcatta cagaatcatc    6940
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390 cgaactctgg ctcgtatgga tcttcaggac cagtcgatca acgaaatgcg ataggccgtc    7060
392 catgcaatga tgacgaaggt gtccgagctc tctcagcgtt cctctcatcc ttcgcctccc    7120
394 actgcgccac ccacaccgcc cgcaccatct tctcctccaa ggggtggttt tcctccggag    7180
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399 <210> SEQ ID NO: 3
400 <211> LENGTH: 21
401 <212> TYPE: PRT
402 <213> ORGANISM: Misgurnus mizolepis
404 <400> SEQUENCE: 3
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406  1               5                  10                  15
408 Glu Ser Ala Pro Gly
409                20
412 <210> SEQ ID NO: 4
413 <211> LENGTH: 28
414 <212> TYPE: PRT
415 <213> ORGANISM: Misgurnus mizolepis
417 <400> SEQUENCE: 4
418 His Arg Cys Pro His Gly Trp Thr Pro Phe Gly Val Gln Cys Tyr Lys
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```
VERIFICATION SUMMARY                     DATE: 01/15/2002
PATENT APPLICATION:  US/10/020,695       TIME: 16:55:54

          Input Set : A:\pto.amc
          Output Set: N:\CRF3\01152002\J020695.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:234 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 2
L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:284 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
```

OIPE

```
                RAW SEQUENCE LISTING              DATE: 01/10/2002
                PATENT APPLICATION:  US/10/020,695   TIME: 15:54:13

                Input Set : A:\ES.txt
                Output Set: N:\CRF3\01102002\J020695.raw
```

Does Not Comply
Corrected Diskette Needed

```
     1 <110> APPLICANT: KIM, Dong-Soo
     2        NAM, Yoon-Kwon
     3        NOH, Jae-Koo
     5 <120> TITLE OF INVENTION: EXPRESSION VECTOR CONTAINING LECTIN GENE REGULATION SITE OF
MUD
     6        LOACH
     8 <130> FILE REFERENCE: PPBA0566
    10 <140> CURRENT APPLICATION NUMBER: US/10/020,695
    10 <141> CURRENT FILING DATE: 2001-12-12
    10 <160> NUMBER OF SEQ ID NOS: 18
    12 <170> SOFTWARE: KopatentIn 1.71
```

ERRORED SEQUENCES

```
   602 <210> SEQ ID NO: 18
   603 <211> LENGTH: 23
   604 <212> TYPE: DNA
   605 <213> ORGANISM: Artificial Sequence
   607 <220> FEATURE:
   608 <223> OTHER INFORMATION: primer for detecting a growth hormone gene of a carp
   611 <400> SEQUENCE: 18
   612 acaacacctg caccagctgg ctg                                          23
E--> 615 1
```

VERIFICATION SUMMARY   DATE: 01/10/2002
PATENT APPLICATION: US/10/020,695   TIME: 15:54:14

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\01102002\J020695.raw**

```
L:10  M:270 C: Current Application Number differs, Replaced Current Application No
L:10  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:234 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 2
L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:284 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:615 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:23 SEQ:18
```